

## **STIC Biotechnology Systems Branch**

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Application Serial Number: 10/516,558A  
Source: PT  
Date Processed by STIC: 3/9/06

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Revised 01/10/06



PCT

## RAW SEQUENCE LISTING

DATE: 03/09/2006

PATENT APPLICATION: US/10/516,558A

TIME: 12:25:13

Input Set : A:\3190-070 Sequence Listing.txt

Output Set : N:\CRF4\03092006\J516558A.raw

3 <110> APPLICANT: Chano, Tokuhiko  
 4 Okabe, Hidetoshi  
 5 Ikegawa, Shiro  
 7 <120> TITLE OF INVENTION: RB1 gene induced protein (RB1CC1) and gene  
 9 <130> FILE REFERENCE: 3190-070  
 11 <140> CURRENT APPLICATION NUMBER: US 10/516,558A  
 12 <141> CURRENT FILING DATE: 2004-11-30  
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00882  
 15 <151> PRIOR FILING DATE: 2003-01-30  
 17 <150> PRIOR APPLICATION NUMBER: JP P2002-161400  
 18 <151> PRIOR FILING DATE: 2002-06-03  
 20 <150> PRIOR APPLICATION NUMBER: JP P2002-214978  
 21 <151> PRIOR FILING DATE: 2002-07-24  
 23 <160> NUMBER OF SEQ ID NOS: 132  
 25 <170> SOFTWARE: PatentIn version 3.1

*pp 1-16, 18*

**Does Not Comply  
Corrected Diskette Needed**

## ERRORED SEQUENCES

27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 1594  
 29 <212> TYPE: PRT  
 30 <213> ORGANISM: Unknown  
 32 <220> FEATURE:  
 33 <223> OTHER INFORMATION: human RB1CC1  
 35 <400> SEQUENCE: 1  
 37 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe  
 38 1 5 10 15  
 41 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile  
 42 20 25 30  
 45 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn  
 46 35 40 45  
 49 Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala  
 50 50 55 60  
 53 Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu  
 54 65 70 75 80  
 E--> 57  
 58 Cys Asp Arg Pro Pro Ala Ile Pro Lys Thr Thr Phe Ser Thr Glu Asn  
 E--> 59 85 90 95  
 62 Asp Met Glu Ile Lys Val Glu Glu Ser Leu Met Met Pro Ala Val Phe  
 E--> 63 100 105 110  
 66 His Thr Val Ala Ser Arg Thr Gln Leu Ala Leu Glu Met Tyr Glu Val  
 E--> 67 115 120 125

-1-

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(global  
error)*

*Per 1.824 of*

*Sequence Rules*

*no page numbers allowed  
IN  
3/9/2006 computer  
readable form*

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70 Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
E--> 71      130      135      140
74 Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
E--> 75 145      150      155      160
78 Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser
E--> 79      165      170      175
82 Asn Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu Thr His Leu
E--> 83      180      185      190
86 Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu Glu Cys Leu
E--> 87      195      200      205
90 Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Leu Asp Ser Leu Pro
E--> 91      210      215      220
94 Glu His Glu Asp Ser Glu Lys Ala Glu Thr Lys Arg Ser Thr Glu Leu
E--> 95 225      230      235      240
98 Val Leu Ser Pro Asp Met Pro Arg Thr Thr Asn Glu Ser Leu Leu Thr
E--> 99      245      250      255
102 Ser Phe Pro Lys Ser Val Glu His Val Ser Pro Asp Thr Ala Asp Ala
E--> 103      260      265      270
106 Glu Ser Gly Lys Glu Ile Arg Glu Ser Cys Gln Ser Thr Val His Gln
E--> 107      275      280      285
110 Gln Asp Glu Thr Thr Ile Asp Thr Lys Asp Gly Asp Leu Pro Phe Phe
E--> 111      290      295      300
E--> 114      -2- delete
116 Asn Val Ser Leu Leu Asp Trp Ile Asn Val Gln Asp Arg Pro Asn Asp
E--> 117 305      310      315      320
120 Val Glu Ser Leu Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp
E--> 121      325      330      335
124 Pro Arg Ile Ile Arg Pro Phe Ile Ala Glu Cys Arg Gln Thr Ile Ala
E--> 125      340      345      350
128 Lys Leu Asp Asn Gln Asn Met Lys Ala Ile Lys Gly Leu Glu Asp Arg
E--> 129      355      360      365
132 Leu Tyr Ala Leu Asp Gln Met Ile Ala Ser Cys Gly Arg Leu Val Asn
E--> 133      370      375      380
136 Glu Gln Lys Glu Leu Ala Gln Gly Phe Leu Ala Asn Gln Lys Arg Ala
E--> 137 385      390      395      400
140 Glu Asn Leu Lys Asp Ala Ser Val Leu Pro Asp Leu Cys Leu Ser His
E--> 141      405      410      415
144 Ala Asn Gln Leu Met Ile Met Leu Gln Asn His Arg Lys Leu Leu Asp
E--> 145      420      425      430
148 Ile Lys Gln Lys Cys Thr Thr Ala Lys Gln Glu Leu Ala Asn Asn Leu
E--> 149      435      440      445
152 His Val Arg Leu Lys Trp Cys Cys Phe Val Met Leu His Ala Asp Gln
E--> 153      450      455      460
156 Asp Gly Glu Lys Leu Gln Ala Leu Leu Arg Leu Val Ile Glu Leu Leu
E--> 157 465      470      475      480
160 Glu Arg Val Lys Ile Val Glu Ala Leu Ser Thr Val Pro Gln Met Tyr
E--> 161      485      490      495
164 Cys Leu Ala Val Val Glu Val Val Arg Lys Met Phe Ile Lys His
E--> 165      500      505      510

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RAW SEQUENCE LISTING  
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Output Set : N:\CRF4\03092006\J516558A.raw

```

168 Tyr Arg Glu Trp Ala Gly Ala Leu Val Lys Asp Gly Lys Arg Leu Tyr
E--> 169          515          520          525
E--> 171
173 Glu Ala Glu Lys Ser Lys Arg Glu Ser Phe Gly Lys Leu Phe Arg Lys
E--> 174          530          535          540
177 Ser Phe Leu Arg Asn Arg Leu Phe Arg Gly Leu Asp Ser Trp Pro Pro
E--> 178 545          550          555          560
181 Ser Phe Cys Thr Gln Lys Pro Arg Lys Phe Asp Cys Glu Leu Pro Asp
E--> 182          565          570          575
185 Ile Ser Leu Lys Asp Leu Gln Phe Leu Gln Ser Phe Cys Pro Ser Glu
E--> 186          580          585          590
189 Val Gln Pro Phe Leu Arg Val Pro Leu Leu Cys Asp Phe Glu Pro Leu
E--> 190          595          600          605
193 His Gln His Val Leu Ala Leu His Asn Leu Val Lys Ala Ala Gln Ser
E--> 194          610          615          620
197 Leu Asp Glu Met Ser Gln Thr Ile Thr Asp Leu Leu Ser Glu Gln Lys
E--> 198 625          630          635          640
201 Ala Ser Val Ser Gln Thr Ser Pro Gln Ser Ala Ser Ser Pro Arg Met
E--> 202          645          650          655
205 Glu Ser Thr Ala Gly Ile Thr Thr Thr Thr Ser Pro Arg Thr Pro Pro
E--> 206          660          665          670
209 Pro Leu Thr Val Gln Asp Pro Leu Cys Pro Ala Val Cys Pro Leu Glu
E--> 210          675          680          685
213 Glu Leu Ser Pro Asp Ser Ile Asp Ala His Thr Phe Asp Phe Glu Thr
E--> 214          690          695          700
217 Ile Pro His Pro Asn Ile Glu Gln Thr Ile His Gln Val Ser Leu Asp
E--> 218 705          710          715          720
221 Leu Asp Ser Leu Ala Glu Ser Pro Glu Ser Asp Phe Met Ser Ala Val
E--> 222          725          730          735
225 Asn Glu Phe Val Ile Glu Glu Asn Leu Ser Ser Pro Asn Pro Ile Ser
E--> 226          740          745          750
E--> 228
229 Asp Pro Gln Ser Pro Glu Met Met Val Glu Ser Leu Tyr Ser Ser Val
E--> 230          755          760          765
233 Ile Asn Ala Ile Asp Ser Arg Arg Met Gln Asp Thr Asn Val Cys Gly
E--> 234          770          775          780
237 Lys Glu Asp Phe Gly Asp His Thr Ser Leu Asn Val Gln Leu Glu Arg
E--> 238 785          790          795          800
241 Cys Arg Val Val Ala Gln Asp Ser His Phe Ser Ile Gln Thr Ile Lys
E--> 242          805          810          815
245 Glu Asp Leu Cys His Phe Arg Thr Phe Val Gln Lys Glu Gln Cys Asp
E--> 246          820          825          830
249 Phe Ser Asn Ser Leu Lys Cys Thr Ala Val Glu Ile Arg Asn Ile Ile
E--> 250          835          840          845
253 Glu Lys Val Lys Cys Ser Leu Glu Ile Thr Leu Lys Glu Lys His Gln
E--> 254          850          855          860
257 Lys Glu Leu Leu Ser Leu Lys Asn Glu Tyr Glu Gly Lys Leu Asp Gly
E--> 258 865          870          875          880
261 Leu Ile Lys Glu Thr Glu Glu Asn Glu Asn Lys Ile Lys Lys Leu Lys

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all  
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TIME: 12:25:13

Input Set : A:\3190-070 Sequence Listing.txt  
Output Set : N:\CRF4\03092006\J516558A.raw

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E--> 262          885          890          895
      265 Gly Glu Leu Val Cys Leu Glu Glu Val Leu Gln Asn Lys Asp Asn Glu
E--> 266          900          905          910
      269 Phe Ala Leu Val Lys His Glu Lys Glu Ala Val Ile Cys Leu Gln Asn
E--> 270          915          920          925
      273 Glu Lys Asp Gln Lys Leu Leu Glu Met Glu Asn Ile Met His Ser Gln
E--> 274          930          935          940
      277 Asn Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Ile Val Leu Glu
E--> 278 945          950          955          960
      281 Asp Leu Lys Lys Leu His Val Glu Asn Asp Glu Lys Leu Gln Leu Leu
E--> 282          965          970          975
E--> 286
      287 Arg Ala Glu Leu Gln Ser Leu Glu Gln Ser His Leu Lys Glu Leu Glu
E--> 288          980          985          990
      291 Asp Thr Leu Gln Val Arg His Ile Gln Glu Phe Glu Lys Val Met Thr
E--> 292          995          1000          1005
      295 Asp His Arg Val Ser Leu Glu Glu Leu Lys Lys Glu Asn Gln Gln
E--> 296          1010          1015          1020
      299 Ile Ile Asn Gln Ile Gln Glu Ser His Ala Glu Ile Ile Gln Glu
E--> 300          1025          1030          1035
      303 Lys Glu Lys Gln Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu
E--> 304          1040          1045          1050
      307 Ser Asp Thr Arg Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu
E--> 308          1055          1060          1065
      311 Ala Glu Thr Asp Glu Ile Lys Ile Leu Leu Glu Glu Ser Arg Ala
E--> 312          1070          1075          1080
      315 Gln Gln Lys Glu Thr Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu
E--> 316          1085          1090          1095
      319 Asn Leu Arg Thr Glu Ile Ser Lys Leu Asn Gln Lys Ile Gln Asp
E--> 320          1100          1105          1110
      323 Asn Asn Glu Asn Tyr Gln Val Gly Leu Ala Glu Leu Arg Thr Leu
E--> 324          1115          1120          1125
      327 Met Thr Ile Glu Lys Asp Gln Arg Ile Ser Glu Leu Ile Ser Arg
E--> 328          1130          1135          1140
      331 His Glu Glu Glu Ser Asn Ile Leu Lys Ala Glu Leu Asn Lys Val
E--> 332          1145          1150          1155
      335 Thr Ser Leu His Asn Gln Ala Phe Glu Ile Glu Lys Asn Leu Lys
E--> 336          1160          1165          1170
      339 Glu Gln Ile Ile Glu Leu Gln Ser Lys Leu Asp Ser Glu Leu Ser
E--> 340          1175          1180          1185
E--> 343
      344 Ala Leu Glu Arg Gln Lys Asp Glu Lys Ile Thr Gln Gln Glu Glu
E--> 345          1190          1195          1200
      348 Lys Tyr Glu Ala Ile Ile Gln Asn Leu Glu Lys Asp Arg Gln Lys
E--> 349          1205          1210          1215
      352 Leu Val Ser Ser Gln Glu Gln Asp Arg Glu Gln Leu Ile Gln Lys
E--> 353          1220          1225          1230
      356 Leu Asn Cys Glu Lys Asp Glu Ala Ile Gln Thr Ala Leu Lys Glu
E--> 357          1235          1240          1245

```

*same  
even*

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Input Set : A:\3190-070 Sequence Listing.txt

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459 <210> SEQ ID NO: 2
460 <211> LENGTH: 1588
461 <212> TYPE: PRT
462 <213> ORGANISM: Unknown
464 <220> FEATURE:
465 <223> OTHER INFORMATION: mouse Rblcc1
467 <400> SEQUENCE: 2
469 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe
470 1 5 10 15
473 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
474 20 25 30
477 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn
478 35 40 45
481 Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala
482 50 55 60
485 Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu
486 65 70 75 80
489 Cys Asp Arg Ala Pro Ala Ile Pro Lys Ala Thr Phe Ser Thr Glu Asn
490 85 90 95
493 Asp Met Glu Ile Lys Val Glu Glu Ser Leu Met Met Pro Ala Val Phe
494 100 105 110
497 His Thr Val Ala Ser Arg Thr Gln Leu Ala Val Glu Met Tyr Asp Val
498 115 120 125
501 Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
502 130 135 140
505 Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
506 145 150 155 160
509 Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser
510 165 170 175
513 Asp Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu Thr His Leu
514 180 185 190
E--> 515
516 Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu Glu Cys Leu
E--> 517 195 200 205
520 Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Pro Asp Ser Leu Asn
E--> 521 210 215 220
524 Glu His Glu Gly Ser Glu Lys Ala Glu Met Lys Arg Ser Thr Glu Leu
E--> 525 225 230 235 240
528 Val Leu Ser Pro Asp Met Pro Arg Thr Thr Asn Thr Ser Leu Val Thr
E--> 529 245 250 255
532 Ser Phe His Lys Ser Met Glu His Val Ala Pro Asp Pro Thr Gly Thr
E--> 533 260 265 270
536 Glu Arg Gly Lys Glu Leu Arg Glu Ser Cys Gln Ser Thr Val Gln Gln
E--> 537 275 280 285
540 Glu Glu Ala Ser Val Asp Ala Lys Asp Ser Asp Leu Pro Phe Phe Asn
E--> 541 290 295 300
544 Val Ser Leu Leu Asp Trp Ile Asn Val Gln Asp Arg Pro Asn Asp Val
E--> 545 305 310 315 320
548 Glu Ser Leu Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp Pro

```

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        647 Ser His Pro Asn Thr Glu Gln Pro Val His Gln Ala Ser Ile Asp Leu
E--> 648 705                      710                      715                      720
        651 Asp Ser Leu Ala Glu Ser Pro Glu Ser Asp Phe Met Ser Ala Val Asn
E--> 652                      725                      730                      735
        655 Glu Phe Val Ile Glu Glu Asn Leu Ser Ser Pro Asn Pro Ile Ser Asp
E--> 656                      740                      745                      750
        660 Pro Gln Ser Pro Glu Met Met Val Glu Ser Leu Tyr Ser Ser Val Ile
E--> 661                      755                      760                      765
        664 Asn Ala Ile Asp Ser Arg Arg Met Gln Asp Thr Ser Thr Arg Gly Asn
E--> 665                      770                      775                      780
        668 Glu Gly Phe Gly Asp Arg Ala Ala Leu His Val Gln Leu Glu Lys Cys
E--> 669 785                      790                      795                      800
        672 Arg Ala Ala Ala Gln Asp Ser His Thr Ser Ile Gln Thr Ile Lys Asp
E--> 673                      805                      810                      815
        676 Asp Leu Cys His Phe Arg Thr Phe Val Gln Lys Glu Gln Cys Asp Leu
E--> 677                      820                      825                      830
        680 Ala Asn Tyr Leu Lys Cys Thr Ala Val Glu Ile Arg Asn Ile Ile Glu
E--> 681                      835                      840                      845
        684 Lys Val Lys Cys Ser Leu Glu Ile Thr Leu Lys Glu Lys His Gln Gln
E--> 685                      850                      855                      860
E--> 687
        688 Glu Leu Gln Ser Leu Lys Ile Glu Tyr Glu Cys Lys Leu Asp Ala Leu
E--> 689 865                      870                      875                      880
        692 Val Lys Asp Ser Glu Glu Asn Val Asn Lys Ile Leu Lys Leu Lys Glu
E--> 693                      885                      890                      895
        696 Asn Leu Val Ser Leu Glu Glu Ala Leu Gln Asn Lys Asp Asn Glu Phe
E--> 697                      900                      905                      910
        700 Thr Ser Ile Lys His Glu Lys Asp Ala Ile Val Cys Val Gln Gln Glu
E--> 701                      915                      920                      925
        705 Lys Asp Gln Lys Leu Leu Glu Met Glu Lys Ile Met His Thr Gln His
E--> 706                      930                      935                      940
        709 Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Met Ala Leu Glu Asp
E--> 710 945                      950                      955                      960
        713 Leu Lys Lys Leu His Asp Glu Lys Ile Glu Ser Leu Arg Ala Glu Phe
E--> 714                      965                      970                      975
        717 Gln Cys Leu Glu Glu Asn His Leu Lys Glu Leu Glu Asp Thr Leu His
E--> 718                      980                      985                      990
        721 Ile Arg His Thr Gln Glu Phe Glu Lys Val Met Thr Asp His Asn Met
E--> 722                      995                      1000                      1005
        725 Ser Leu Glu Lys Leu Lys Lys Glu Asn Gln Gln Arg Ile Asp Gln
E--> 726                      1010                      1015                      1020
        730 Met Leu Glu Ser His Ala Ser Thr Ile Gln Glu Lys Glu Gln Gln
E--> 731                      1025                      1030                      1035
        734 Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu Ser Asp Met Arg
E--> 735                      1040                      1045                      1050
        738 Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu Ala Glu Thr Asp
E--> 739                      1055                      1060                      1065
        742 Glu Ile Lys Ile Leu Leu Glu Glu Ser Arg Thr Gln Gln Lys Glu
E--> 743                      1070                      1075                      1080

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-12-

*same*

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E--> 549          325          330          335
      552 Lys Ile Ile Gln Pro Phe Met Leu Glu Cys His Gln Thr Ile Ala Lys
E--> 553          340          345          350
      556 Leu Asp Asn Gln Asn Met Lys Ala Ile Lys Gly Leu Glu Asp Arg Leu
E--> 557          355          360          365
      560 Tyr Ala Leu Asp Gln Met Ile Ala Ser Cys Ser Arg Leu Val Asn Glu
E--> 561          370          375          380
      564 Gln Lys Glu Leu Ala Gln Gly Phe Leu Ala Asn Gln Met Arg Ala Glu
E--> 565 385          390          395          400
      568 Asn Leu Lys Asp Ala Ser Val Leu Pro Asp Leu Cys Leu Ser His Ala
E--> 569          405          410          415
E--> 572          -10-
      573 Asn Gln Leu Met Ile Met Leu Gln Asn His Arg Lys Leu Leu Asp Ile
E--> 574          420          425          430
      577 Lys Gln Lys Cys Thr Thr Ala Lys Gln Glu Leu Ala Asn Asn Leu His
E--> 578          435          440          445
      581 Val Arg Leu Lys Trp Cys Cys Phe Val Met Leu His Ala Asp Gln Asp
E--> 582          450          455          460
      585 Gly Glu Lys Leu Gln Ala Leu Leu Arg Leu Val Ile Glu Leu Leu Glu
E--> 586 465          470          475          480
      589 Arg Val Arg Ile Val Glu Ala Leu Ser Thr Val Pro Gln Met Tyr Cys
E--> 590          485          490          495
      593 Leu Ala Val Val Glu Val Val Arg Arg Lys Met Phe Ile Lys His Tyr
E--> 594          500          505          510
      597 Arg Glu Trp Ala Gly Ala Leu Val Lys Asp Gly Lys Gln Leu Tyr Glu
E--> 598          515          520          525
      601 Ala Glu Lys Ser Lys Arg Glu Ser Phe Gly Lys Leu Phe Arg Lys Ser
E--> 602          530          535          540
      605 Phe Leu Arg Asn Arg Leu Phe Lys Gly Leu Asp Ser Trp Pro Ser Ser
E--> 606 545          550          555          560
      609 Phe Cys Thr Gln Lys Pro Arg Lys Phe Asp Cys Glu Leu Pro Asp Ile
E--> 610          565          570          575
      613 Ser Leu Lys Asp Leu Gln Phe Leu Gln Ser Phe Cys Pro Ser Glu Val
E--> 614          580          585          590
      617 Gln Pro Phe Leu Arg Val Pro Leu Leu Cys Asp Phe Glu Pro Leu His
E--> 618          595          600          605
      621 Gln His Val Leu Ala Leu His Asn Leu Val Lys Ala Ala Gln Ser Leu
E--> 622          610          615          620
      625 Asp Glu Met Ser Gln Thr Ile Thr Asp Leu Leu Asn Glu Gln Lys Val
E--> 626 625          630          635          640
E--> 628          -11-
      631 Ser Thr Ser Gln Ala Ser Pro Gln Ser Ala Ala Ser Pro Arg Ile Glu
E--> 632          645          650          655
      635 Ser Thr Thr Gly Ile Thr Thr Thr Thr Ser Pro Lys Thr Pro Pro Pro
E--> 636          660          665          670
      639 Leu Thr Val Gln Asp Thr Leu Cys Pro Ala Val Cys Pro Leu Glu Glu
E--> 640          675          680          685
      643 Leu Ser Pro Asp Ser Ile Asp Ala His Thr Phe Asp Phe Glu Thr Ile
E--> 644          690          695          700

```

*same  
even*



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360 Phe Lys Leu Glu Arg Glu Val Val Glu Lys Glu Leu Leu Glu Lys
E--> 361      1250      1255      1260
364 Val Lys His Leu Glu Asn Gln Ile Ala Lys Ser Pro Ala Ile Asp
E--> 365      1265      1270      1275
368 Ser Thr Arg Gly Asp Ser Ser Ser Leu Val Ala Glu Leu Gln Glu
E--> 369      1280      1285      1290
372 Lys Leu Gln Glu Glu Lys Ala Lys Phe Leu Glu Gln Leu Glu Glu
E--> 373      1295      1300      1305
376 Gln Glu Lys Arg Lys Asn Glu Glu Met Gln Asn Val Arg Thr Ser
E--> 377      1310      1315      1320
380 Leu Ile Ala Glu Gln Gln Thr Asn Phe Asn Thr Val Leu Thr Arg
E--> 381      1325      1330      1335
384 Glu Lys Met Arg Lys Glu Asn Ile Ile Asn Asp Leu Ser Asp Lys
E--> 385      1340      1345      1350
388 Leu Lys Ser Thr Met Gln Gln Gln Glu Arg Asp Lys Asp Leu Ile
E--> 389      1355      1360      1365
392 Glu Ser Leu Ser Glu Asp Arg Ala Arg Leu Leu Glu Glu Lys Lys
E--> 393      1370      1375      1380
396 Lys Leu Glu Glu Glu Val Ser Lys Leu Arg Ser Ser Ser Phe Val
E--> 397      1385      1390      1395
E--> 401
      -7-
402 Pro Ser Pro Tyr Val Ala Thr Ala Pro Glu Leu Tyr Gly Ala Cys
E--> 403      1400      1405      1410
406 Ala Pro Glu Leu Pro Gly Glu Ser Asp Arg Ser Ala Val Glu Thr
E--> 407      1415      1420      1425
410 Ala Asp Glu Gly Arg Val Asp Ser Ala Met Glu Thr Ser Met Met
E--> 411      1430      1435      1440
414 Ser Val Gln Glu Asn Ile His Met Leu Ser Glu Glu Lys Gln Arg
E--> 415      1445      1450      1455
418 Ile Met Leu Leu Glu Arg Thr Leu Gln Leu Lys Glu Glu Asn
E--> 419      1460      1465      1470
422 Lys Arg Leu Asn Gln Arg Leu Met Ser Gln Ser Met Ser Ser Val
E--> 423      1475      1480      1485
426 Ser Ser Arg His Ser Glu Lys Ile Ala Ile Arg Asp Phe Gln Val
E--> 427      1490      1495      1500
430 Gly Asp Leu Val Leu Ile Ile Leu Asp Glu Arg His Asp Asn Tyr
E--> 431      1505      1510      1515
434 Val Leu Phe Thr Val Ser Pro Thr Leu Tyr Phe Leu His Ser Glu
E--> 435      1520      1525      1530
438 Ser Leu Pro Ala Leu Asp Leu Lys Pro Gly Glu Gly Ala Ser Gly
E--> 439      1535      1540      1545
442 Ala Ser Arg Arg Pro Trp Val Leu Gly Lys Val Met Glu Lys Glu
E--> 443      1550      1555      1560
446 Tyr Cys Gln Ala Lys Lys Ala Gln Asn Arg Phe Lys Val Pro Leu
E--> 447      1565      1570      1575
450 Gly Thr Lys Phe Tyr Arg Val Lys Ala Val Ser Trp Asn Lys Lys
E--> 451      1580      1585      1590
454 Val
E--> 458
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*same*

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Input Set : A:\3190-070 Sequence Listing.txt  
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E--> 744  
 745 Met Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu Asn Leu Arg Thr  
 E--> 746 1085 1090 1095  
 749 Glu Ile Ser Lys Leu Asn Gln Lys Ile His Asp Asn Asn Glu Ser  
 E--> 750 1100 1105 1110  
 753 Tyr Gln Val Gly Leu Ser Glu Leu Arg Ala Leu Met Thr Ile Glu  
 E--> 754 1115 1120 1125  
 758 Lys Asp Gln Cys Ile Ser Glu Leu Ile Ser Arg His Glu Glu Glu  
 E--> 759 1130 1135 1140  
 762 Ser Asn Ile Leu Lys Ala Glu Leu Asp Asn Val Thr Ser Leu His  
 E--> 763 1145 1150 1155  
 766 Arg Gln Ala Tyr Glu Ile Glu Lys Lys Leu Lys Glu Gln Ile Val  
 E--> 767 1160 1165 1170  
 770 Glu Leu Gln Thr Arg Leu Asn Ser Glu Leu Ser Ala Leu Glu Lys  
 E--> 771 1175 1180 1185  
 774 Gln Lys Asp Glu Lys Ile Thr Gln Gln Glu Glu Lys Tyr Glu Ala  
 E--> 775 1190 1195 1200  
 778 Leu Ile Gln Asn Leu Glu Lys Asp Lys Glu Arg Leu Val Lys Asn  
 E--> 779 1205 1210 1215  
 782 His Glu Gln Asp Lys Glu His Leu Ile Gln Glu Leu Asn Phe Glu  
 E--> 783 1220 1225 1230  
 786 Lys Asn Lys Ala Val Gln Thr Ala Leu Asp Glu Phe Lys Val Glu  
 E--> 787 1235 1240 1245  
 790 Arg Glu Leu Val Glu Lys Glu Leu Leu Glu Lys Val Lys His Leu  
 E--> 791 1250 1255 1260  
 794 Glu Asn Gln Ile Ala Lys Thr Pro Ala Phe Glu Ser Ala Arg Glu  
 E--> 795 1265 1270 1275  
 798 Asp Ser Ser Ser Leu Val Ala Glu Leu Gln Glu Lys Leu Gln Glu  
 E--> 799 1280 1285 1290  
 E--> 802  
 803 Glu Lys Ala Lys Phe Leu Glu Gln Leu Glu Glu Gln Glu Lys Arg  
 E--> 804 1295 1300 1305  
 807 Lys Asn Glu Glu Met Gln Asn Val Arg Thr Ser Leu Ile Ala Glu  
 E--> 808 1310 1315 1320  
 811 Gln Gln Thr Asn Phe Asn Thr Val Leu Thr Arg Glu Lys Met Arg  
 E--> 812 1325 1330 1335  
 815 Lys Glu Asn Ile Ile Asn Asp Leu Ser Asp Lys Leu Lys Ser Thr  
 E--> 816 1340 1345 1350  
 819 Met Gln Gln Gln Glu Arg Asp Lys Asp Leu Ile Glu Ser Leu Ser  
 E--> 820 1355 1360 1365  
 823 Glu Asp Arg Ala Arg Leu Leu Glu Glu Lys Lys Gln Leu Glu Glu  
 E--> 824 1370 1375 1380  
 827 Glu Val Ser Lys Leu Arg Thr Ser Ser Phe Leu Ser Ser Ala Pro  
 E--> 828 1385 1390 1395  
 831 Val Ala Ala Ala Pro Glu Leu Tyr Gly Ala Cys Ala Pro Glu Leu  
 E--> 832 1400 1405 1410  
 835 Pro Gly Glu Pro Glu Arg Ser Val Met Glu Thr Ala Asp Glu Gly  
 E--> 836 1415 1420 1425  
 839 Arg Leu Asp Ser Ala Met Glu Thr Ser Met Met Ser Val Gln Glu

*same*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006  
TIME: 12:25:13

Input Set : A:\3190-070 Sequence Listing.txt  
Output Set: N:\CRF4\03092006\J516558A.raw

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E--> 840      1430      1435      1440
      843 Asn Met  Leu Ser Glu Glu Lys  Gln Arg Ile Met  Leu  Leu Glu Arg
E--> 844      1445      1450      1455
      847 Thr Leu  Gln Leu Lys Glu Glu  Glu Asn Lys Arg  Leu  Asn Gln Arg
E--> 848      1460      1465      1470
      851 Leu Met  Ser Gln Ser Leu Ser  Ser Val Ser Ser  Arg  His Ser Glu
E--> 852      1475      1480      1485
      855 Lys Ile  Ala Ile Arg Asp Phe  Gln Val Gly Asp  Leu  Val Leu Ile
E--> 856      1490      1495      1500
E--> 858
      861 Ile Leu  Asp Glu Arg His Asp  Asn Tyr Val Leu  Phe  Thr Val Ser
E--> 862      1505      1510      1515
      865 Pro Thr  Leu Tyr Phe Leu His  Ser Glu Ser Leu  Pro  Ala Leu Asp
E--> 866      1520      1525      1530
      868 Leu Lys  Pro Gly Glu Gly Ala  Ser Gly Ala Ser  Arg  Arg Pro Trp
E--> 869      1535      1540      1545
      871 Val Leu  Gly Lys Val Met Glu  Lys Glu Tyr Cys  Gln  Ala Lys Lys
E--> 872      1550      1555      1560
      875 Ala Gln  Asn Arg Phe Lys Val  Pro Leu Gly Thr  Lys  Phe Tyr Arg
E--> 876      1565      1570      1575
      879 Val Lys  Ala Val Ser Trp Asn  Lys Lys Val
E--> 880      1580      1585
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      883 <211> LENGTH: 6636
      884 <212> TYPE: DNA
      885 <213> ORGANISM: Unknown
      887 <220> FEATURE:
      888 <223> OTHER INFORMATION: human RB1CC1 gene
      890 <400> SEQUENCE: 3
      891 gtcgacaata acaaaccaag ccgcggcgggt gtccgcggcc ctgcccagcc ctcggcgttg      60
      893 cctcagaatc cccagtcgc ctgggccct cggctctgac aggccgcggc cttctgtccc      120
      895 ccggcccccag acccagagcc gaggggcctg ctcgctcct tgtccgcccg gacccctccc      180
      897 tgccctctag agttcggggc cgcggcgggc gggcgcccgg gacgcggcgg gttgtgtcgg      240
      899 cttagcgggt ccgaatgggc ggttggtaac cgctgccgag gactaggcgg cggcgggaaga      300
      901 tgggtgccggg ggtcgtggc tctgctgctg ccgcccggca aggaggaggc gttgccgggt      360
      903 ttctgagttt aaccagtaat gccattcagt tgccaatctc aagcaaagca aacataagcc      420
      905 agttttaatc tactttttaa gaaaagtggg agtccttttc acagtgcctg acgtaactgt      480
      907 atcagagggg gaggtataag ctcacagaat tcagataaat catcatgaag ttatatgtat      540
      909 ttctggttaa cactggaact actctaact ttgacactga acttacagtg caaactgtgg      600
      911 cagaccttaa gcatgccatt caaagcaaat acaagattgc tattcaacac cagggtgctg      660
      913 tggccaatgg aggagaatgc atggctgcag atcgaagcgt gtgtacctac agtgctggga      720
E--> 915
      918 cggatacaaaa tccaattttt ctttttaaca aagaaatgat cttatgcgat cgtccacctg      780
      920 ctattcctaa aactaccttt tcgacagaaa atgacatgga aataaaaagt gaagaatctc      840
      922 ttatgatgcc tgcagttttt catactgttg cttcaaggac acagcttgca ttggaaatgt      900
      924 atgaagtgc caagaaactt tgttcttttt gtgaaggctc tgtacatgat gaacatcttc      960
      926 aacaccaagg ctgggctgca atcatggcca acctggagga ctgttcaaat tcatacaaaa      1020
      928 agctactttt caagtttgaa agtatattatt caaattatct gcagtccata gaagacatca      1080
      930 agttaaaact tactcattta ggaactgcag tttcagtaat ggccaagatt ccactgttgg      1140

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 PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006  
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932	agtgcctaac	cagacatagt	tacagagaat	gtttgggaag	actggattct	ttacctgaac	1200
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936	tgccatagaac	aactaacgaa	tctttgttaa	cctcatttcc	caagtcagtg	gaacatgtgt	1320
938	ccccagatac	cgcagatgct	gaaagtggca	aagaaattag	ggaatcttgt	caaagtactg	1380
940	ttcatcagca	agatgaaact	acgattgaca	ctaaagatgg	tgatctgccc	ttttttaatg	1440
942	tctctttgtt	agactggata	aatgttcaag	atagacctaa	tgatgtggaa	tctttggtca	1500
944	ggaagtgcct	tgattctatg	agcaggcttg	atccaaggat	tattcgacca	tttatagcag	1560
946	aatgccgtca	aactattgcc	aaacttgata	atcagaatat	gaaagccatt	aaaggacttg	1620
948	aagatcggct	ctacgccctg	gaccagatga	ttgctagctg	tggccgactg	gtgaatgaac	1680
950	agaaagagct	tgctcagga	tttttagcta	atcagaagag	agctgaaaac	ttaaaggatg	1740
952	catctgtatt	acctgattta	tgctgagtc	acgcaaata	gttgatgatt	atgttgcaaa	1800
954	atcatagaaa	actgttagat	attaagcaga	agtgtaccac	tgccaaacaa	gaactagcaa	1860
956	ataacctaca	tgtcagactg	aagtgggtgt	gctttgtaat	gcttcagtgt	gatcaaatg	1920
958	gagagaagtt	acaagctttg	ctccgcctcg	taataagact	gttagaaaaga	gtcaaaattg	1980
960	ttgaagctct	tagtacagtt	cctcagatgt	actgcttagc	tggtgttgag	gttgtaagaa	2040
962	gaaaaatgtt	cataaaacac	tacagggagt	gggctggtgc	tttagtcaaa	gatggaaaga	2100
964	gattatatga	agcagaaaaa	tcaaaaagg	aatcctttgg	gaaattattt	aggaagtctt	2160
966	ttttaagaaa	tcgtctgttt	aggggactgg	actcctggcc	cccttccttt	tgtactcaaa	2220
968	agcctcgaaa	gtttgactgt	gaacttcag	atatttcatt	aaaagattta	cagtttctgc	2280
970	aatcattttg	tccttcggaa	gttcagccat	tcctcagggt	tccttactt	tgtgactttg	2340
972	aacctctaca	ccagcatgta	cttgctctac	ataatttgg	aaaagcagca	caaagtttgg	2400
E--> 974				-17-	same		
975	atgaaatgtc	acagaccatt	acagatctac	tgagtgaaca	aaaggcatct	gtgagccaga	2460
977	catccccaca	gtctgcttct	tcaccaagga	tggaaagtac	agcaggaatt	acaactacta	2520
979	cctcaccgag	aactcctcca	ccactgactg	ttcaggatcc	cttatgtcct	gcagtttgtc	2580
981	ccttagaaga	attatctcca	gatagtattg	atgcacatac	gtttgatttt	gaaactattc	2640
983	cccatccaaa	catagaacag	actattcacc	aagtttcttt	agacttggat	tcattagcag	2700
985	aaagtcttga	atcagatttt	atgtctgctg	tgaatgagtt	tgtaatagaa	gaaaatttgt	2760
987	cgtctcctaa	tcctataagt	gatccacaaa	gccagaaaat	gatggtggaa	tcactttatt	2820
989	catcagttat	caatgcgata	gacagttagc	gaatgcagga	tacaaatgta	tgtggtaagg	2880
991	aggattttgg	agatcatact	tctctgaatg	tccagttgga	aagatgtaga	gttggtgccc	2940
993	aagactctca	cttcagtata	caaaccatta	aggaagacct	ttgccacttt	agaacatttg	3000
995	tacaaaaaga	acagtgtgac	ttctcaaatt	cattaaaatg	tacagcagta	gaaataagaa	3060
997	acattattga	aaaagtaaaa	tgttctctgg	aaataacact	aaaagaaaaa	catcaaaaag	3120
999	aactactgtc	tttaaaaaat	gaatatgaag	gtaaacttga	cggactaata	aaggaaactg	3180
1001	aagagaatga	aaacaaaatt	aaaaaattga	agggagagtt	agtatgcctt	gaggaggttt	3240
1003	tacaaaataa	agataatgaa	tttgctttgg	ttaaacatga	aaaagaagct	gtaatctgcc	3300
1005	tgcagaatga	aaaggatcag	aagttgtag	agatggaaaa	tataatgcac	tctcaaaatt	3360
1007	gtgaaattaa	agaactgaag	cagtcacgag	aaatagtgtt	agaagactta	aaaaagctcc	3420
1009	atgttgaaaa	tgatgagaag	ttacagttaa	tgagggcgaa	acttcagtcc	ttggagcaaa	3480
1011	gtcatctaaa	ggaattagag	gacacacttc	aggttaggca	catacaagag	tttgagaagg	3540
1013	ttatgacaga	ccacagagtt	tctttggagg	aattaaaaaa	ggaaaatcaa	caaataatta	3600
1015	atcaaataca	agaatctcat	gctgaaatta	tccaggaaaa	agaaaaacag	ttacaggaat	3660
1017	taaaactcaa	ggtttctgat	ttgtcagaca	cgagatgcaa	gttagagggt	gaacttgctg	3720
1019	tgaaggaagc	agaaactgat	gaaataaaaa	ttttgctgga	agaaagcaga	gccagcaga	3780
1021	aggagacctt	gaaatctctt	cttgaacaag	agacagaaaa	tttgagaaca	gaaattagta	3840
1023	aactcaacca	aaagattcag	gataataatg	aaaattatca	ggtgggctta	gcagagctaa	3900
1025	gaactttaat	gacaattgaa	aaagatcagc	gtatttcgga	gttaattagt	agacatgaag	3960
1027	aagaatctaa	tataacttaa	gctgaattaa	acaaagtaac	atctttgcat	aaccaagcat	4020

RAW SEQUENCE LISTING  
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DATE: 03/09/2006  
TIME: 12:25:13

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1029 ttgaaataga aaaaaaccta aaagaacaaa taattgaact gcagagtaaa ttggattcag 4080
E--> 1031 -18- same
1032 aattgagtgc tcttgaaaga caaaaagatg aaaaaattac ccaacaagaa gagaaatacg 4140
1034 aagctattat ccagaacctt gagaaagaca gacaaaaatt ggtagcagc caggagcaag 4200
1036 acagagaaca gttaattcag aagcttaatt gtgaaaaaga tgaagctatt cagactgccc 4260
1038 taaaagaatt taaattggag agagaagtgt ttgagaaaga gttattagaa aaagttaaag 4320
1040 atcttgagaa tcaaatagca aaaaagtcctg ccattgactc taccagagga gattcctcaa 4380
1042 gcttagttgc tgaacttcaa gaaaagcttc aggaagaaaa agctaagttt ctagaacaac 4440
1044 ttgaagagca agaaaaaaga aagaatgaag aaatgcaaaa tgttcgaaca tctttgattg 4500
1046 cggaacaaca gaccaatttt aacactgttt taacaagaga gaaaatgaga aaagaaaaca 4560
1048 taataaatga tcttagtgat aagttgaaaa gtacaatgca gcaacaagaa cgggataaag 4620
1050 atttgataga gtcactttct gaagatcgag ctggtttgct tgaggaaaag aaaaagcttg 4680
1052 aagaagaagt cagtaagttg cgcagtagca gttttgttcc ttcaccatat gtagctacag 4740
1054 cccagaact ttatggagct tgtgcacctg aactcccagg tgaatcagat agatccgtg 4800
1056 tggaaacagc agatgaagga agagtggatt cagcaatgga gacaagcatg atgtctgtac 4860
1058 aagaaaaat tcatatgttg tctgaagaaa aacagcggat aatgctgtta gaacgaacat 4920
1060 tgcaattgaa agaagaagaa aataaacggg taaatcaaag actgatgtct cagagcatgt 4980
1062 cttcagtatc ttcaaggcat tctgaaaaga tagctattag agattttcag gtgggagatt 5040
1064 tggtagtcat catcctagac gaacgccatg acaattatgt gttatttact gttagtccta 5100
1066 ctttatattt tctacattca gagtctctac ctgccctgga tctcaaacca ggtgaggggtg 5160
1068 cttcaggtgc atctagaaga ccctgggtac ttggaaaagt aatggaaaaa gaatactgtc 5220
1070 aagccaaaaa ggcacaaaac agatttaaag ttcctttggg gacaaaagtt tacagagtga 5280
1072 aagccgtatc atggaataag aaagtataac ttatggacaa aattaatata ttctatgaca 5340
1074 tttttttctg atttgtcctg cagtgtcat tcatcactcc aaaaacagca ggccatcttt 5400
1076 ttatgcaaaa gtcagcgtga caatatactt cactgggtga catcgtttac tttttaactg 5460
1078 gcttcatttt aggaataata aattcatcag aatccttggc tgaattaaaa tggtttttgt 5520
1080 tttttggttt ttttttttac ccagacaact ctagaaatgc ggaccaaaact acttcatttt 5580
1082 ctcaaaagggc ataccttggtg cattgtggct tatgatgagc catattaatt gcctgttaaa 5640
1084 tatacactag cttgaactta gatgttaa tttatttata ccagcatttg tctttttgtg 5700
1086 aatcagtat cagaatactt gcactcttta acacattctt tataaaatgt ataaattatt 5760
E--> 1088 -19-
1089 cagaactatt taaaataaag aggagtgtta ttgcatgctg ataatcattt tgagtttgcc 5820
1091 tcagtagata ctaaagcaaa ttgtttcagt ttttttaaat gccctttgat gtttcaaaaa 5880
1093 aaaaaaggaa ctgtaatttg attgactgat tttaagatca gccataagta atcagcaatc 5940
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1113 taattctttt tcagaaaata ttttaatttct tcataaaaaat aagttaaata tttttttaaa 6540
1115 tatgtatatc taatagtaca aaatggaata aacatcatag tgtatagaaa actgaatttg 6600
1117 acaagttaat gaataaatga acaaatgatt tcaaaa 6636
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1121 <211> LENGTH: 6518
1122 <212> TYPE: DNA

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PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006

TIME: 12:25:13

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1123 &lt;213&gt; ORGANISM: Unknown

1125 &lt;220&gt; FEATURE:

1126 &lt;223&gt; OTHER INFORMATION: mouse Rblcc1 gene

1128 &lt;400&gt; SEQUENCE: 4

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1131	cctcggccgg	cggactcggg	tccccgcgcg	gagccgaggg	gccggagcag	cggctgcgcc	120
1133	cgactcccat	ccttcggggc	ctcgccgggt	actcggcggc	tgggcgccga	cggttgtgtc	180
1135	ggttgccggc	gccgcagggg	cggttgatag	ccgccgccga	ggccagggcg	gcggcagaag	240
1137	atggtgcgga	gggcccggcg	ctgtgttgct	gccgcggggc	gaggaggcgc	tgccggttct	300
1139	ctgagtttca	ccagtaatgc	cactcagttg	ccaatatcaa	gcaagcgcac	ataagacaat	360
1141	tgtaatcttt	taagaaaagt	agtacttctc	ttcacagtat	ctggcggatc	aacactggag	420
1143	ggtgaggtgt	cagcttcag	aaagatcatc	atgaagttat	atgtgtttct	ggttaacacc	480

E--&gt; 1145

1146	ggaaccacgc	tgacatttga	cactgagcta	actgtgcaaa	ctgtggctga	tcttaagcat	540
1148	gccattcaaa	gcaaatacaa	gatttgctatt	cagcaccagg	ttctggtggt	caatggagga	600
1150	gaatgcatgg	ctgcagatcg	aagagtgtgt	acttacagcg	ctgggacgga	cacaaatcca	660
1152	atttttcttt	ttaataaaga	aatgatctta	tgtgaccgtg	cacctgctat	tcctaaagct	720
1154	accttttcaa	cagaaaatga	catggaaata	aaagttgaag	agtctcttat	gatgcctgca	780
1156	gttttccaca	ctgttgcttc	aaggacacag	cttgacgtgg	aaatgtatga	cgttgccaag	840
1158	aagctctgct	ctttctgtga	agggcttgct	catgatgaac	atcttcagca	ccaaggctgg	900
1160	gctgcaatca	tggccaatct	ggaggactgt	tcaaattcat	acaaaaaact	tcttttcaag	960
1162	tttgaaagta	tttattctga	ttatcttcaa	tccatagaag	acatcaagtt	aaaacttact	1020
1164	catttaggaa	ctgctgtttc	agtaatggcc	aagattccac	tattggagtg	cctaaccaga	1080
1166	catagttaca	gggaatgttt	gggaagaccg	gattctttga	atgaacatga	aggctcagag	1140
1168	aaagctgaga	tgaaaagatc	tactgaactg	gtgctctctc	ctgatatgcc	tagaacaacg	1200
1170	aacacatcct	tggtaacctc	atttcacaag	tcaatggagc	atgtagctcc	agatcccacc	1260
1172	ggtactgaac	gtggcaaaga	acttagggaa	tcttgtcaaa	gtactgtcca	gcaagaagaa	1320
1174	gcttcagtgg	atgctaaaga	cagtgatctg	ccttttttta	atgtttcttt	gttagactgg	1380
1176	ataaatgttc	aagatagacc	caatgatgtg	gaatctctgg	tcaggaagtg	ctttgattct	1440
1178	atgagcaggc	ttgaccctaa	gattattcaa	ccatttatgt	tagaatgcca	tcaaaactatt	1500
1180	gccaaaacttg	ataatcagaa	tatgaaagcc	attaaagggc	ttgaagatcg	gctgtatgcc	1560
1182	ttggaccaga	tgattgctag	ctgtagccgg	ctggtaaaatg	aacagaaaaga	gcttgctcag	1620
1184	ggatttttag	ctaatacagat	gagagctgaa	aacttgaaag	atgcatctgt	gttacctgat	1680
1186	ctgtgtctga	gtcatgcaaa	tcaactaatg	attatgttgc	aaaaccacag	aaaactgttg	1740
1188	gatattaaac	agaagtgcac	cactgccaaa	caagagctag	caaacaatct	ccacgtcaga	1800
1190	ctgaagtggg	gttggtttgt	gatgcttcat	gctgatcaag	atggagaaaa	actgcaggca	1860
1192	ctgctccgcc	ttgtaataga	gctgttagaa	agagtcagaa	ttgttgaggc	tcttagtaca	1920
1194	gttcctcaga	tgtattgcct	agctgttggt	gaggttgtaa	gaagaaaaat	gttcattaaa	1980
1196	cactacagag	agtgggctgg	tgctttagtc	aaagacggaa	aacaactata	tgaagctgaa	2040
1198	aagtcaaaaa	gggaatcctt	tgggaaatta	tttaggaagt	cctttttaag	aaatcgctctg	2100
1200	tttaaaggac	tggactcctg	gccttcctca	ttttgtactc	agaagcctcg	aaaatttgac	2160

E--&gt; 1202

1203	tgtgaacttc	cagatatatc	attaaaagat	ttacagtttc	ttcaatcatt	ttgtccttca	2220
1205	gaagtgcagc	catttcctcag	ggtcccctta	ctttgtgact	ttgaacctct	acaccagcat	2280
1207	gtacttgccc	tacataattt	ggtaaaagca	gcacaaagtt	tggatgaaat	gtcacagact	2340
1209	attacagatc	tcttaaataga	acaaaaggta	tccacaagtc	aggcatcccc	acagtcagct	2400
1211	gcttctccaa	gaatagaaaag	tacaacaggc	attacaacca	ctacctcacc	aaaaactcct	2460
1213	cctccactaa	ctgttcagga	caccttatgt	ccggcagtg	gtcccttaga	agaattatct	2520
1215	ccagatagta	tcgatgctca	tacatttgat	ttcgaaacca	tctcccatcc	aaacacagaa	2580

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006  
TIME: 12:25:13

Input Set : A:\3190-070 Sequence Listing.txt  
Output Set: N:\CRF4\03092006\J516558A.raw

1217	caacctgttc	accaagcttc	tatagacttg	gattcattag	cagaaagccc	tgagtctgac	2640
1219	tttatgtctg	ctgtgaatga	gtttgtgata	gaagaaaatt	tatcgtctcc	aaaccctata	2700
1221	agtgatccac	aaagtccaga	aatgatggtg	gagtcacttt	actcttcagt	catcaatgca	2760
1223	atagatagta	ggcgtatgca	agacacaagt	acacgtggaa	acgagggcct	tggggatcgg	2820
1225	gctgctctac	atgtccagct	ggagaaatgc	agagctgctg	cacaagactc	tcacaccagt	2880
1227	atacaaacca	tcaaggacga	tctgtgccat	ttcagaacat	ttgtacaaaa	agaacagtgt	2940
1229	gacttagcaa	attattttaa	atgtacagct	gtagaaataa	gaaatattat	tgaaaaagta	3000
1231	aaatgttctc	tagaaataac	actaaaggaa	aagcatcagc	agaactcca	atcttttaaa	3060
1233	attgagtatg	aatgtaaact	tgatgctcta	gtaaaagaca	gtgaagaaaa	tgtaataaaa	3120
1235	atttttaaa	tgaagaaaa	tttagtatcc	cttgaagagg	ctttacaaaa	taaagacaat	3180
1237	gaattcactt	cgattaaaca	tgaaaaggat	gctattgtct	gtgtgcagca	agaaaaggat	3240
1239	cagaagttgt	tagagatgga	aaagataatg	catactcaac	attgtgaaat	taaagaactg	3300
1241	aagcagtcac	gagagatggc	attagaagac	ctgaaaaagc	tgcatgatga	aaaaactcag	3360
1243	tcattgagag	ctgaatttca	gtgcttagaa	gaaaatcacc	tgaaggaatt	agaggacaca	3420
1245	ctgcacatca	ggcacacaca	ggagtttgag	aaagttatga	cagaccacaa	tatgtctttg	3480
1247	gagaaattaa	aaaaagaaaa	tcagcaaaga	attgaccaga	tgctagaatc	tcatgcctca	3540
1249	actattcagg	aaaaagagca	acagctgcag	gagttgaaac	tcaaagtttc	tgacttgtca	3600
1251	gacatgagat	gtaagttaga	ggttgaactt	gcactaaagg	aagcagaaac	agatgagata	3660
1253	aagatcttgt	tggaagagag	cagaacacag	cagaaggaaa	tgctgaagtc	tttacttgaa	3720
1255	caagagaccg	aaaacttaag	aacagaaata	agtaactaa	acaaaaaat	tcatgataat	3780
1257	aatgagagtt	accaggtggg	tttgtcagag	tttagagctt	taatgacaat	tgaaaaagat	3840
E--> 1259				-22-	same		
1260	cagtgcattt	cagagttaat	cagtagacat	gaagaagaat	ctaataact	taaggctgaa	3900
1262	ttagacaatg	ttacatcttt	gcacgcgcaa	gcataatgaa	tagaaaaaaa	actgaaagaa	3960
1264	caaatagttg	aattgcagac	tagattgaac	tcagaattga	gtgctcttga	aaaacagaaa	4020
1266	gatgaaaaaa	ttaccaaca	agaagagaag	tatgaagcac	ttatccagaa	ccttgagaaa	4080
1268	gacaaggaga	gactggtcaa	gaaccacgag	caagacaaag	aacacttaat	tcaggagctt	4140
1270	aattttgaaa	aaaacaaagc	tgttcaaact	gcactagatg	aatttaaggt	ggagagagaa	4200
1272	cttggttgaga	aagagttatt	agaaaaggtt	aaacatcttg	agaatcaaat	agccaaaact	4260
1274	cctgcctttg	agtcagccag	agaagattct	tcaagcttag	ttgcggaact	tcaagagaaa	4320
1276	cttcaagaag	aaaaagctaa	gtttctggaa	caacttgaag	aacaagagaa	aagaaagaat	4380
1278	gaggaaatgc	aaaatgtcag	aacctctttg	attgctgagc	agcagaccaa	ctttaacaca	4440
1280	gtcttaacaa	gagagaaaat	gaggaaagaa	aacataataa	atgatcttag	tgataagcta	4500
1282	aaaagtacaa	tgacgcagca	agagcgggat	aaagatttga	tagagtcgct	ctctgaggac	4560
1284	cgagctcggt	tgcttgaaga	gaagaagcag	cttgaagagg	aagtgaagta	actccgact	4620
1286	agcagttttc	tttcctcagc	acctgtggct	gcagcccag	agctctatgg	tgctgtgca	4680
1288	cctgagctcc	caggggagcc	agagagatca	gtcatggaga	cggcagatga	aggaagactg	4740
1290	gattccgcaa	tgagacaag	catgatgtct	gtccaagaaa	acatgttatc	tgaagagaag	4800
1292	cagaggatca	tgctcctaga	acggacattg	cagttgaaag	aagaagaaaa	caagcggtta	4860
1294	aatcaaagac	tgatgtctca	gagtttgtcc	tcagtctctt	caaggcattc	tgaaaaata	4920
1296	gccattagag	attttcaggt	gggagatttg	gttctcatca	tcctagatga	gcggcacgac	4980
1298	aattatgtat	tgtttactgt	tagtctact	ttatattttc	tgactcaga	gtctcttct	5040
1300	gccctggatc	tcaaaccagg	tgaggagcct	tcaggtgcat	ctagaagacc	ctgggtcctt	5100
1302	gggaaagtaa	tggaagga	atactgtcaa	gccaaaagg	cacaaaacag	atttaaagtt	5160
1304	cctttgggga	caaagtttta	cagagtgaag	gctgtgtcat	ggaataagaa	agtatagcca	5220
1306	cagaagaaat	ctctacatct	cataccattt	ttgatttgtc	ctccagtgtc	gataaactac	5280
1308	tctaaaaaca	gctggccatt	gttgggtttt	ttttgttgt	ttgtttgttt	gtttgttttt	5340
1310	acaaaagtca	acataacaat	atacttcatt	gggtgactgc	acttaccttt	taagtggcta	5400
1312	catcttagga	acaataaatt	tattaaaatt	cttggctgaa	tcaaaatggt	tttgttttgt	5460

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/516,558A

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Input Set : A:\3190-070 Sequence Listing.txt  
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1314 ttccacccaa ataactagaa attcggacca aaatagatgt tttccaaggg cagagcctgc 5520  
E--> 1316 *-23- pp 24-25 also appear (but not shown on this page)*  
1317 actgtggcct gtgactagcc tcattagttg cctgttaata aacattagct gaatagttac 5580  
1319 cagtgttggt accagcattt gtcctcttgt gaattcaaga gtcctcgac tctttaacat 5640  
1321 gttctttata aaatgtataa acccttccaa actattttaa gaggagtgtt attgcatgca 5700  
1323 gataatcata attttgagtt tgcctcagaa gactactaaa gcaaatttgt tcattttttt 5760  
1325 ttaaaaaaat gccctttaat gtttcaaaaa aaaataacag tgtaatttga ctgactttta 5820  
1327 gatcagccat aaataatgag cagtcttcaa aagcactttt cacacagatc atctgggctc 5880  
1329 cagggaggaa gagtctgtgc cactgatgtt ttcaagtgc ggactcactc aaacctctca 5940  
1331 gcacttagg actgtttcaa gtaatcata tgatgaactc gtaattcatg gttgaccttc 6000  
1333 agaagaagat attcattgta tattaacatt tagaggtcat ttaataaca aaagtctgta 6060  
1335 ttgtaaagga cctgtacaat tttaagacaa taaagaattg aaagtgtaaa tgtgtgtgcc 6120  
1337 ttttaaaggt tacattttta atatttgcg tgatttctgg gaaagggtgaa aaaaatgttc 6180  
1339 tgtatcaaa agaaacctgt ttattaaaa atgttgtttg tatcctatgt aacagggtga 6240  
1341 agtgggtgttc tgtggaacag aaccatgtaa actcaaggtt taaaagctgg cactgaacaa 6300  
1343 agatattgaa gtagctaggc tagttgattg gaaagagttt cttcagggtt gttgttagca 6360  
1345 gtaataaatg attctttttc agaaatattt aatttctcca taaaaataag ttggatattt 6420  
1347 ttataaatat gtaatcta ataatgaaaa tgggaataaac atagtgtata gaatacctaa 6480  
1349 ttcaaaaaa tattaatgaa taaacgaaca aatgatta 6518

1475 <210> SEQ ID NO: 15

1476 <211> LENGTH: 21

1477 <212> TYPE: DNA

1478 <213> ORGANISM: Artificial

1480 <220> FEATURE:

1481 <223> OTHER INFORMATION: artificially synthesized primer sequence called

CC1-S8

1483 <400> SEQUENCE: 15

1484 aaggaagacc ttgcccatt t

21

E--> 1487

1645 <210> SEQ ID NO: 29

1646 <211> LENGTH: 20

1647 <212> TYPE: DNA

1648 <213> ORGANISM: Artificial

1650 <220> FEATURE:

1651 <223> OTHER INFORMATION: artificially synthesized primer sequence called

RB1CC-R3

1653 <400> SEQUENCE: 29

1654 aaactcagaa aaccggcaac

20

E--> 1657

1818 <210> SEQ ID NO: 43

1819 <211> LENGTH: 20

1820 <212> TYPE: DNA

1821 <213> ORGANISM: Artificial

1823 <220> FEATURE:

1824 <223> OTHER INFORMATION: artificially synthesized primer sequence called

MMK1-2-S

1826 <400> SEQUENCE: 43

1827 taagcatgcc attcaaagca

20

E--> 1830

1990 <210> SEQ ID NO: 57

1991 <211> LENGTH: 20

1992 <212> TYPE: DNA



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006  
TIME: 12:25:14

Input Set : A:\3190-070 Sequence Listing.txt  
Output Set: N:\CRF4\03092006\J516558A.raw

1993 <213> ORGANISM: Artificial  
1995 <220> FEATURE:  
1996 <223> OTHER INFORMATION: artificially synthesized primer sequence called  
MCC-S8  
1998 <400> SEQUENCE: 57  
1999 acgtggcaaa gaacttaggg 20  
E--> 2003  
2161 <210> SEQ ID NO: 71  
2162 <211> LENGTH: 20  
2163 <212> TYPE: DNA  
2164 <213> ORGANISM: Artificial  
2166 <220> FEATURE:  
2167 <223> OTHER INFORMATION: artificially synthesized primer sequence called  
MCC-AS3  
2169 <400> SEQUENCE: 71  
2170 tgccgctcat ctaggatgat 20  
E--> 2174  
2394 <210> SEQ ID NO: 90  
2395 <211> LENGTH: 20  
2396 <212> TYPE: DNA  
2397 <213> ORGANISM: Artificial  
2399 <220> FEATURE:  
2400 <223> OTHER INFORMATION: artificially synthesized primer sequence called  
MINT2-S0  
2402 <400> SEQUENCE: 90  
2403 tgccactcag ttgccaagta 20  
E--> 2404  
2564 <210> SEQ ID NO: 104  
2565 <211> LENGTH: 20  
2566 <212> TYPE: DNA  
2567 <213> ORGANISM: Artificial  
2569 <220> FEATURE:  
2570 <223> OTHER INFORMATION: artificially synthesized primer sequence called  
MINT9-AS  
2572 <400> SEQUENCE: 104  
2573 gcctgcagtt tttctccatc 20  
E--> 2576  
2738 <210> SEQ ID NO: 118  
2739 <211> LENGTH: 20  
2740 <212> TYPE: DNA  
2741 <213> ORGANISM: Artificial  
2743 <220> FEATURE:  
2744 <223> OTHER INFORMATION: artificially synthesized primer sequence called  
MINT16-AS  
2746 <400> SEQUENCE: 118  
2747 gctcttgctg ctgcattgta 20  
E--> 2751  
2910 <210> SEQ ID NO: 132  
2911 <211> LENGTH: 20  
2912 <212> TYPE: DNA  
2913 <213> ORGANISM: Artificial  
2915 <220> FEATURE:  
2916 <223> OTHER INFORMATION: artificially synthesized primer sequence called

MINT23-AS

2918 <400> SEQUENCE: 132

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006

TIME: 12:25:14

Input Set : A:\3190-070 Sequence Listing.txt

Output Set: N:\CRF4\03092006\J516558A.raw

2919 cagcactgga ggacaaatca

E--> 2922

-51-

also 49-50

20

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006

TIME: 12:25:15

Input Set : A:\3190-070 Sequence Listing.txt

Output Set: N:\CRF4\03092006\J516558A.raw

L:57 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1  
M:332 Repeated in SeqNo=1  
L:515 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
M:332 Repeated in SeqNo=2  
L:915 M:254 E: No. of Bases conflict, this line has no nucleotides.  
M:254 Repeated in SeqNo=3  
L:1145 M:254 E: No. of Bases conflict, this line has no nucleotides.  
M:254 Repeated in SeqNo=4  
L:1374 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1430 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:  
L:1487 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:1545 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1601 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:  
L:1602 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1657 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:1717 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1773 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:  
L:1774 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1830 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:1888 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1945 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:  
L:2003 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:2061 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2117 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:  
L:2118 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2174 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:2232 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2290 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:  
L:2291 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2347 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:2404 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:2518 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:  
L:2519 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2576 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:2638 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2694 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:  
L:2695 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2751 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:2809 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2865 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:  
L:2866 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2922 M:254 E: No. of Bases conflict, this line has no nucleotides.